

RECEIVED

MAY 25 2001

TECH CENTER 1600/2900

SEQUENCE LISTING



<110> Otsuka Pharmaceutical Co., Ltd.

<120> HUMAN P51 GENES AND GENE PRODUCTS THEREOF

<130> Q61014

<140> 09/670,568

<141> 2000-09-27

<150> JP 10-100467

<151> 1998-03-27

<160> 23

<170> PatentIn version 3.0

<210> 1

<211> 448

<212> PRT

<213> Homo sapiens

<220>

<221> DOMAIN

<222> (1)..(59)

<223> transactivation domain

<220>

<221> DNA_BIND

<222> (142)..(321)

<223> DNA binding domain

<220>

<221> DOMAIN

<222> (353)..(397)

<223> oligomerization domain

<400> 1

Met Ser Gln Ser Thr Gln Thr Asn Glu Phe Leu Ser Pro Glu Val Phe
1 5 10 15

Gln His Ile Trp Asp Phe Leu Glu Gln Pro Ile Cys Ser Val Gln Pro
20 25 30

Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp Gly Ala Thr Asn
35 40 45

Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu
50 55 60

Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser
 65 70 75 80
 Met Asp Gln Gln Ile Gln Asn Gly Ser Ser Ser Thr Ser Pro Tyr Asn
 85 90 95
 Thr Asp His Ala Gln Asn Ser Val Thr Ala Pro Ser Pro Tyr Ala Gln
 100 105 110
 Pro Ser Ser Thr Phe Asp Ala Leu Ser Pro Ser Pro Ala Ile Pro Ser
 115 120 125
 Asn Thr Asp Tyr Pro Gly Pro His Ser Phe Asp Val Ser Phe Gln Gln
 130 135 140
 Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Thr Glu Leu Lys
 145 150 155 160
 Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val
 165 170 175
 Met Thr Pro Pro Pro Gln Gly Ala Val Ile Arg Ala Met Pro Val Tyr
 180 185 190
 Lys Lys Ala Glu His Val Thr Glu Val Val Lys Arg Cys Pro Asn His
 195 200 205
 Glu Leu Ser Arg Glu Phe Asn Glu Gly Gln Ile Ala Pro Pro Ser His
 210 215 220
 Leu Ile Arg Val Glu Gly Asn Ser His Ala Gln Tyr Val Glu Asp Pro
 225 230 235 240
 Ile Thr Gly Arg Gln Ser Val Leu Val Pro Tyr Glu Pro Pro Gln Val
 245 250 255
 Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys Asn Ser Ser
 260 265 270
 Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Val Thr Leu
 275 280 285
 Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Cys Phe Glu Ala Arg
 290 295 300
 Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile
 305 310 315 320
 Arg Lys Gln Gln Val Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys
 325 330 335
 Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys
 340 345 350
 Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly

aac ctg ggg ctc ctg aac agc atg gac cag cag att cag aac ggc tcc Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn Gly Ser 75 80 85	411
tcg tcc acc agt ccc tat aac aca gac cac gcg cag aac agc gtc acg Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser Val Thr 90 95 100 105	459
gcg ccc tcg ccc tac gca cag ccc agc tcc acc ttc gat gct ctc tct Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala Leu Ser 110 115 120	507
cca tca ccc gcc atc ccc tcc aac acc gac tac cca ggc ccg cac agt Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His Ser 125 130 135	555
ttc gac gtg tcc ttc cag cag tcg agc acc gcc aag tcg gcc acc tgg Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp 140 145 150	603
acg tat tcc act gaa ctg aag aaa ctc tac tgc caa att gca aag aca Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr 155 160 165	651
D7 tgc ccc atc cag atc aag gtg atg acc cca cct cct cag gga gct gtt Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly Ala Val 170 175 180 185	699
atc cgc gcc atg cct gtc tac aaa aaa gct gag cac gtc acg gag gtg Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Glu Val 190 195 200	747
At wt gtg aag cgg tgc ccc aac cat gag ctg agc cgt gaa ttc aac gag gga Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn Glu Gly 205 210 215	795
cag att gcc cct cct agt cat ttg att cga gta gag ggg aac agc cat Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn Ser His 220 225 230	843
gcc cag tat gta gaa gat ccc atc aca gga aga cag agt gtg ctg gta Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val Leu Val 235 240 245	891
cct tat gag cca ccc cag gtt ggc act gaa ttc acg aca gtc ttg tac Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val Leu Tyr 250 255 260 265	939
aat ttc atg tgt aac agc agt tgt gtt gga ggg atg aac cgc cgt cca Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro 270 275 280	987
att tta atc att gtt act ctg gaa acc aga gat ggg caa gtc ctg ggc Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val Leu Gly 285 290 295	1035

cga cgc tgc ttt gag gcc cgg atc tgt gct tgc cca gga aga gac agg	1083
Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg	
300 305 310	
aag gcg gat gaa gat agc atc aga aag cag caa gtt tcg gac agt aca	1131
Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp Ser Thr	
315 320 325	
aag aac ggt gat ggt acg aag cgc ccg ttt cgt cag aac aca cat ggt	1179
Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr His Gly	
330 335 340 345	
atc cag atg aca tcc atc aag aaa cga aga tcc cca gat gat gaa ctg	1227
Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp Glu Leu	
350 355 360	
tta tac tta cca gtg agg ggc cgt gag act tat gaa atg ctg ttg aag	1275
Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu Leu Lys	
365 370 375	
atc aaa gag tcc ctg gaa ctc atg cag tac ctt cct cag cac aca att	1323
Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His Thr Ile	
380 385 390	
gaa acg tac agg caa cag caa cag cag cag cac cag cac tta ctt cag	1371
Glu Thr Tyr Arg Gln Gln Gln Gln Gln Gln His Gln His Leu Leu Gln	
395 400 405	
aaa cat ctc ctt tca gcc tgc ttc agg aat gag ctt gtg gag ccc cgg	1419
Lys His Leu Leu Ser Ala Cys Phe Arg Asn Glu Leu Val Glu Pro Arg	
410 415 420 425	
aga gaa act cca aaa caa tct gac gtc ttc ttt aga cat tcc aag ccc	1467
Arg Glu Thr Pro Lys Gln Ser Asp Val Phe Phe Arg His Ser Lys Pro	
430 435 440	
cca aac cga tca gtg tac cca tagagcccta tctctatatt ttaagtgtgt	1518
Pro Asn Arg Ser Val Tyr Pro	
445	
gtgttggtatt tccatgtgta tatgtgagtg tgtgtgtgtg tatgtgtgtg cgtgtgtatc	1578
tagccctcat aaacaggact tgaagacact ttggctcaga gacccaactg ctcaaaggca	1638
caaagccact agtgagagaa tcttttgaag ggactcaaac ctttacaaga aaggatgttt	1698
tctgcagatt ttgtatcctt agaccggcca ttggtgggtg aggaaccact gtgtttgtct	1758
gtgagctttc tgttgtttcc tgggagggag gggtcaggtg gggaaagggg cattaagatg	1818
tttattggaa cccttttctg tcttcttctg ttgtttttct aaaattcaca gggaagcttt	1878
tgagcaggtc tcaaacttaa gatgtctttt taagaaaagg agaaaaaagt tgttattgtc	1938

tgtgcataag taagttgtag gtgactgaga gactcagtca gaccctttta atgctgggtca 1998
 tgtaataata ttgcaagtag taagaaacga aggtgtcaag tgtactgctg ggcagcgagg 2058
 tgatcattac caaaagtaat caactttgtg ggtggagagt tctttgtgag aacttgcatt 2118
 atttgtgtcc tcccctcatg tgtaggtaga acatttctta atgctgtgta cctgcctctg 2178
 ccactgtatg ttggcatctg ttatgctaaa gtttttcttg tacatgaaac cctggaagac 2238
 ctactacaaa aaaactgttg tttggcccc atagcaggtg aactcatttt gtgcttttaa 2298
 tagaaagaca aatccacccc agtaatatg cccttacgta gttgtttacc attattcaaa 2358
 gctcaaaata gaatttgaag ccctctcaca aaatctgtga ttaatttgct taattagagc 2418
 ttctatccct caagcctacc taccataaaa ccagccatat tactgatact gttcagtgca 2478
 tttagccagg agacttacgt tttgagtaag tgagatccaa gcagacgtgt taaaatcagc 2538
 actcctggac tggaaattaa agattgaaag ggtagactac ttttcttttt tttactcaaa 2598
 agtttagaga atctctgttt ctttccattt taaaaacata ttttaagata atagcataaa 2658
 gactttaaaa atgttccctc cctccatctt cccacacca gtcaccagca ctgtattttc 2718
 tgtcaccaag acaatgattt cttgttattg aggctgttgc ttttgtggat gtgtgatttt 2778
 aattttcaat aaacttttgc atcttggttt aaaagaaa 2816

<210> 3
 <211> 448
 <212> PRT
 <213> Homo sapiens
 <400> 3

Met Ser Gln Ser Thr Gln Thr Asn Glu Phe Leu Ser Pro Glu Val Phe
 1 5 10 15
 Gln His Ile Trp Asp Phe Leu Glu Gln Pro Ile Cys Ser Val Gln Pro
 20 25 30
 Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp Gly Ala Thr Asn
 35 40 45
 Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu
 50 55 60
 Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser
 65 70 75 80
 Met Asp Gln Gln Ile Gln Asn Gly Ser Ser Ser Thr Ser Pro Tyr Asn
 85 90 95

Thr Asp His Ala Gln Asn Ser Val Thr Ala Pro Ser Pro Tyr Ala Gln
 100 105 110
 Pro Ser Ser Thr Phe Asp Ala Leu Ser Pro Ser Pro Ala Ile Pro Ser
 115 120 125
 Asn Thr Asp Tyr Pro Gly Pro His Ser Phe Asp Val Ser Phe Gln Gln
 130 135 140
 Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Thr Glu Leu Lys
 145 150 155 160
 Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val
 165 170 175
 Met Thr Pro Pro Pro Gln Gly Ala Val Ile Arg Ala Met Pro Val Tyr
 180 185 190
 Lys Lys Ala Glu His Val Thr Glu Val Val Lys Arg Cys Pro Asn His
 195 200 205
 Glu Leu Ser Arg Glu Phe Asn Glu Gly Gln Ile Ala Pro Pro Ser His
 210 215 220
 Leu Ile Arg Val Glu Gly Asn Ser His Ala Gln Tyr Val Glu Asp Pro
 225 230 235 240
 Ile Thr Gly Arg Gln Ser Val Leu Val Pro Tyr Glu Pro Pro Gln Val
 245 250 255
 Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys Asn Ser Ser
 260 265 270
 Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Val Thr Leu
 275 280 285
 Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Cys Phe Glu Ala Arg
 290 295 300
 Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile
 305 310 315 320
 Arg Lys Gln Gln Val Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys
 325 330 335
 Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys
 340 345 350
 Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly
 355 360 365
 Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu
 370 375 380

Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln
385 390 395 400

Gln Gln Gln His Gln His Leu Leu Gln Lys His Leu Leu Ser Ala Cys
405 410 415

Phe Arg Asn Glu Leu Val Glu Pro Arg Arg Glu Thr Pro Lys Gln Ser
420 425 430

Asp Val Phe Phe Arg His Ser Lys Pro Pro Asn Arg Ser Val Tyr Pro
435 440 445

<210> 4
<211> 641
<212> PRT
<213> Homo sapiens

<220>
<221> DOMAIN
<222> (1)..(59)
<223> transactivation domain

D7
<220>
<221> DNA_BIND
<222> (142)..(321)
<223> DNA binding domain

A/Cmt
<220>
<221> DOMAIN
<222> (353)..(397)
<223> oligomerization domain

<400> 4

Met Ser Gln Ser Thr Gln Thr Asn Glu Phe Leu Ser Pro Glu Val Phe
1 5 10 15

Gln His Ile Trp Asp Phe Leu Glu Gln Pro Ile Cys Ser Val Gln Pro
20 25 30

Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp Gly Ala Thr Asn
35 40 45

Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu
50 55 60

Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser
65 70 75 80

Met Asp Gln Gln Ile Gln Asn Gly Ser Ser Ser Thr Ser Pro Tyr Asn
85 90 95

Thr Asp His Ala Gln Asn Ser Val Thr Ala Pro Ser Pro Tyr Ala Gln
 100 105 110
 Pro Ser Ser Thr Phe Asp Ala Leu Ser Pro Ser Pro Ala Ile Pro Ser
 115 120 125
 Asn Thr Asp Tyr Pro Gly Pro His Ser Phe Asp Val Ser Phe Gln Gln
 130 135 140
 Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Thr Glu Leu Lys
 145 150 155 160
 Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val
 165 170 175
 Met Thr Pro Pro Pro Gln Gly Ala Val Ile Arg Ala Met Pro Val Tyr
 180 185 190
 Lys Lys Ala Glu His Val Thr Glu Val Val Lys Arg Cys Pro Asn His
 195 200 205
 Glu Leu Ser Arg Glu Phe Asn Glu Gly Gln Ile Ala Pro Pro Ser His
 210 215 220
 Leu Ile Arg Val Glu Gly Asn Ser His Ala Gln Tyr Val Glu Asp Pro
 225 230 235 240
 Ile Thr Gly Arg Gln Ser Val Leu Val Pro Tyr Glu Pro Pro Gln Val
 245 250 255
 Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys Asn Ser Ser
 260 265 270
 Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Val Thr Leu
 275 280 285
 Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Cys Phe Glu Ala Arg
 290 295 300
 Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile
 305 310 315 320
 Arg Lys Gln Gln Val Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys
 325 330 335
 Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys
 340 345 350
 Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly
 355 360 365
 Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu
 370 375 380
 Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln

385 390 395 400
 Gln Gln Gln His Gln His Leu Leu Gln Lys Gln Thr Ser Ile Gln Ser
 405 410 415
 Pro Ser Ser Tyr Gly Asn Ser Ser Pro Pro Leu Asn Lys Met Asn Ser
 420 425 430
 Met Asn Lys Leu Pro Ser Val Ser Gln Leu Ile Asn Pro Gln Gln Arg
 435 440 445
 Asn Ala Leu Thr Pro Thr Thr Ile Pro Asp Gly Met Gly Ala Asn Ile
 450 455 460
 Pro Met Met Gly Thr His Met Pro Met Ala Gly Asp Met Asn Gly Leu
 465 470 475 480
 Ser Pro Thr Gln Ala Leu Pro Pro Pro Leu Ser Met Pro Ser Thr Ser
 485 490 495
 His Cys Thr Pro Pro Pro Pro Tyr Pro Thr Asp Cys Ser Ile Val Ser
 500 505 510
 Phe Leu Ala Arg Leu Gly Cys Ser Ser Cys Leu Asp Tyr Phe Thr Thr
 515 520 525
 Gln Gly Leu Thr Thr Ile Tyr Gln Ile Glu His Tyr Ser Met Asp Asp
 530 535 540
 Leu Ala Ser Leu Lys Ile Pro Glu Gln Phe Arg His Ala Ile Trp Lys
 545 550 555 560
 Gly Ile Leu Asp His Arg Gln Leu His Glu Phe Ser Ser Pro Ser His
 565 570 575
 Leu Leu Arg Thr Pro Ser Ser Ala Ser Thr Val Ser Val Gly Ser Ser
 580 585 590
 Glu Thr Arg Gly Glu Arg Val Ile Asp Ala Val Arg Phe Thr Leu Arg
 595 600 605
 Gln Thr Ile Ser Phe Pro Pro Arg Asp Glu Trp Asn Asp Phe Asn Phe
 610 615 620
 Asp Met Asp Ala Arg Arg Asn Lys Gln Gln Arg Ile Lys Glu Glu Gly
 625 630 635 640
 Glu

<210> 5
 <211> 2270
 <212> DNA
 <213> Homo sapiens

<220>

<221> exon

<222> (145) .. (2067)

<400> 5

tcgttgatat caaagacagt tgaaggaaat gaattttgaa acttcacggt gtgccaccct 60

acagtactgc cctgaccctt acatccagcg tttcgtagaa acccagctca tttctcttgg 120

aaagaaagtt attaccgatc cacc atg tcc cag agc aca cag aca aat gaa 171

Met Ser Gln Ser Thr Gln Thr Asn Glu

1

5

ttc ctc agt cca gag gtt ttc cag cat atc tgg gat ttt ctg gaa cag 219

Phe Leu Ser Pro Glu Val Phe Gln His Ile Trp Asp Phe Leu Glu Gln

10

15

20

25

cct ata tgt tca gtt cag ccc att gac ttg aac ttt gtg gat gaa cca 267

Pro Ile Cys Ser Val Gln Pro Ile Asp Leu Asn Phe Val Asp Glu Pro

30

35

40

tca gaa gat ggt gcg aca aac aag att gag att agc atg gac tgt atc 315

Ser Glu Asp Gly Ala Thr Asn Lys Ile Glu Ile Ser Met Asp Cys Ile

45

50

55

cgc atg cag gac tcg gac ctg agt gac ccc atg tgg cca cag tac acg 363

Arg Met Gln Asp Ser Asp Leu Ser Asp Pro Met Trp Pro Gln Tyr Thr

60

65

70

aac ctg ggg ctc ctg aac agc atg gac cag cag att cag aac ggc tcc 411

Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn Gly Ser

75

80

85

tcg tcc acc agt ccc tat aac aca gac cac gcg cag aac agc gtc acg 459

Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser Val Thr

90

95

100

105

gcg ccc tcg ccc tac gca cag ccc agc tcc acc ttc gat gct ctc tct 507

Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala Leu Ser

110

115

120

cca tca ccc gcc atc ccc tcc aac acc gac tac cca ggc ccg cac agt 555

Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His Ser

125

130

135

ttc gac gtg tcc ttc cag cag tcg agc acc gcc aag tcg gcc acc tgg 603

Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp

140

145

150

acg tat tcc act gaa ctg aag aaa ctc tac tgc caa att gca aag aca 651

Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr

155

160

165

tgc ccc atc cag atc aag gtg atg acc cca cct cct cag gga gct gtt 699

Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly Ala Val

170	175	180	185	
atc cgc gcc atg cct gtc tac aaa aaa gct gag cac gtc acg gag gtg Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Glu Val	190	195	200	747
gtg aag cgg tgc ccc aac cat gag ctg agc cgt gaa ttc aac gag gga Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn Glu Gly	205	210	215	795
cag att gcc cct cct agt cat ttg att cga gta gag ggg aac agc cat Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn Ser His	220	225	230	843
gcc cag tat gta gaa gat ccc atc aca gga aga cag agt gtg ctg gta Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val Leu Val	235	240	245	891
cct tat gag cca ccc cag gtt ggc act gaa ttc acg aca gtc ttg tac Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val Leu Tyr	250	255	260	939
aat ttc atg tgt aac agc agt tgt gtt gga ggg atg aac cgc cgt cca Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro	270	275	280	987
att tta atc att gtt act ctg gaa acc aga gat ggg caa gtc ctg ggc Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val Leu Gly	285	290	295	1035
cga cgc tgc ttt gag gcc cgg atc tgt gct tgc cca gga aga gac agg Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg	300	305	310	1083
aag gcg gat gaa gat agc atc aga aag cag caa gtt tcg gac agt aca Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp Ser Thr	315	320	325	1131
aag aac ggt gat ggt acg aag cgc ccg ttt cgt cag aac aca cat ggt Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr His Gly	330	335	340	1179
atc cag atg aca tcc atc aag aaa cga aga tcc cca gat gat gaa ctg Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp Glu Leu	350	355	360	1227
tta tac tta cca gtg agg ggc cgt gag act tat gaa atg ctg ttg aag Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu Leu Lys	365	370	375	1275
atc aaa gag tcc ctg gaa ctc atg cag tac ctt cct cag cac aca att Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His Thr Ile	380	385	390	1323
gaa acg tac agg caa cag caa cag cag cag cac cag cac tta ctt cag				1371

Glu	Thr	Tyr	Arg	Gln	Gln	Gln	Gln	Gln	Gln	His	Gln	His	Leu	Leu	Gln	
395						400					405					
aaa	cag	acc	tca	ata	cag	tct	cca	tct	tca	tat	ggg	aac	agc	tcc	cca	1419
Lys	Gln	Thr	Ser	Ile	Gln	Ser	Pro	Ser	Ser	Tyr	Gly	Asn	Ser	Ser	Pro	
410					415					420					425	
cct	ctg	aac	aaa	atg	aac	agc	atg	aac	aag	ctg	cct	tct	gtg	agc	cag	1467
Pro	Leu	Asn	Lys	Met	Asn	Ser	Met	Asn	Lys	Leu	Pro	Ser	Val	Ser	Gln	
				430					435					440		
ctt	atc	aac	cct	cag	cag	cgc	aac	gcc	ctc	act	cct	aca	acc	att	cct	1515
Leu	Ile	Asn	Pro	Gln	Gln	Arg	Asn	Ala	Leu	Thr	Pro	Thr	Thr	Ile	Pro	
				445				450						455		
gat	ggc	atg	gga	gcc	aac	att	ccc	atg	atg	ggc	acc	cac	atg	cca	atg	1563
Asp	Gly	Met	Gly	Ala	Asn	Ile	Pro	Met	Met	Gly	Thr	His	Met	Pro	Met	
		460					465					470				
gct	gga	gac	atg	aac	gga	ctc	agc	ccc	acc	cag	gca	ctc	cct	ccc	cca	1611
Ala	Gly	Asp	Met	Asn	Gly	Leu	Ser	Pro	Thr	Gln	Ala	Leu	Pro	Pro	Pro	
	475					480					485					
ctc	tcc	atg	cca	tcc	acc	tcc	cac	tgc	aca	ccc	cca	cct	ccg	tat	ccc	1659
Leu	Ser	Met	Pro	Ser	Thr	Ser	His	Cys	Thr	Pro	Pro	Pro	Pro	Tyr	Pro	
490					495					500					505	
aca	gat	tgc	agc	att	gtc	agt	ttc	tta	gcg	agg	ttg	ggc	tgt	tca	tca	1707
Thr	Asp	Cys	Ser	Ile	Val	Ser	Phe	Leu	Ala	Arg	Leu	Gly	Cys	Ser	Ser	
				510					515					520		
tgt	ctg	gac	tat	ttc	acg	acc	cag	ggg	ctg	acc	acc	atc	tat	cag	att	1755
Cys	Leu	Asp	Tyr	Phe	Thr	Thr	Gln	Gly	Leu	Thr	Thr	Ile	Tyr	Gln	Ile	
				525				530					535			
gag	cat	tac	tcc	atg	gat	gat	ctg	gca	agt	ctg	aaa	atc	cct	gag	caa	1803
Glu	His	Tyr	Ser	Met	Asp	Asp	Leu	Ala	Ser	Leu	Lys	Ile	Pro	Glu	Gln	
		540					545					550				
ttt	cga	cat	gcg	atc	tgg	aag	ggc	atc	ctg	gac	cac	cgg	cag	ctc	cac	1851
Phe	Arg	His	Ala	Ile	Trp	Lys	Gly	Ile	Leu	Asp	His	Arg	Gln	Leu	His	
	555					560					565					
gaa	ttc	tcc	tcc	cct	tct	cat	ctc	ctg	cgg	acc	cca	agc	agt	gcc	tct	1899
Glu	Phe	Ser	Ser	Pro	Ser	His	Leu	Leu	Arg	Thr	Pro	Ser	Ser	Ala	Ser	
570					575					580					585	
aca	gtc	agt	gtg	ggc	tcc	agt	gag	acc	cgg	ggg	gag	cgt	gtt	att	gat	1947
Thr	Val	Ser	Val	Gly	Ser	Ser	Glu	Thr	Arg	Gly	Glu	Arg	Val	Ile	Asp	
				590					595					600		
gct	gtg	cga	ttc	acc	ctc	cgc	cag	acc	atc	tct	ttc	cca	ccc	cga	gat	1995
Ala	Val	Arg	Phe	Thr	Leu	Arg	Gln	Thr	Ile	Ser	Phe	Pro	Pro	Arg	Asp	
			605					610						615		

gag tgg aat gac ttc aac ttt gac atg gat gct cgc cgc aat aag caa 2043
 Glu Trp Asn Asp Phe Asn Phe Asp Met Asp Ala Arg Arg Asn Lys Gln
 620 625 630

cag cgc atc aaa gag gag ggg gag tgagcctcac catgtgagct cttcctatcc 2097
 Gln Arg Ile Lys Glu Glu Gly Glu
 635 640

ctctcctaac tgccagcccc ctaaaagcac tcctgcttaa tcttcaaagc cttctcccta 2157

gctcctcccc ttcctcttgt ctgatttctt aggggaagga gaagtaagag gctacctctt 2217

acctaacatc tgacctggca tctaattctg attctggctt taagccttca aaa 2270

<210> 6
 <211> 641
 <212> PRT
 <213> Homo sapiens

<400> 6

Met Ser Gln Ser Thr Gln Thr Asn Glu Phe Leu Ser Pro Glu Val Phe
 1 5 10 15

Gln His Ile Trp Asp Phe Leu Glu Gln Pro Ile Cys Ser Val Gln Pro
 20 25 30

Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp Gly Ala Thr Asn
 35 40 45

Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu
 50 55 60

Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser
 65 70 75 80

Met Asp Gln Gln Ile Gln Asn Gly Ser Ser Ser Thr Ser Pro Tyr Asn
 85 90 95

Thr Asp His Ala Gln Asn Ser Val Thr Ala Pro Ser Pro Tyr Ala Gln
 100 105 110

Pro Ser Ser Thr Phe Asp Ala Leu Ser Pro Ser Pro Ala Ile Pro Ser
 115 120 125

Asn Thr Asp Tyr Pro Gly Pro His Ser Phe Asp Val Ser Phe Gln Gln
 130 135 140

Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Thr Glu Leu Lys
 145 150 155 160

Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val
 165 170 175

Met Thr Pro Pro Pro Gln Gly Ala Val Ile Arg Ala Met Pro Val Tyr
 180 185 190
 Lys Lys Ala Glu His Val Thr Glu Val Val Lys Arg Cys Pro Asn His
 195 200 205
 Glu Leu Ser Arg Glu Phe Asn Glu Gly Gln Ile Ala Pro Pro Ser His
 210 215 220
 Leu Ile Arg Val Glu Gly Asn Ser His Ala Gln Tyr Val Glu Asp Pro
 225 230 235 240
 Ile Thr Gly Arg Gln Ser Val Leu Val Pro Tyr Glu Pro Pro Gln Val
 245 250 255
 Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys Asn Ser Ser
 260 265 270
 Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Val Thr Leu
 275 280 285
 Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Cys Phe Glu Ala Arg
 290 295 300
 Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile
 305 310 315 320
 Arg Lys Gln Gln Val Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys
 325 330 335
 Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys
 340 345 350
 Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly
 355 360 365
 Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu
 370 375 380
 Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln
 385 390 395 400
 Gln Gln Gln His Gln His Leu Leu Gln Lys Gln Thr Ser Ile Gln Ser
 405 410 415
 Pro Ser Ser Tyr Gly Asn Ser Ser Pro Pro Leu Asn Lys Met Asn Ser
 420 425 430
 Met Asn Lys Leu Pro Ser Val Ser Gln Leu Ile Asn Pro Gln Gln Arg
 435 440 445
 Asn Ala Leu Thr Pro Thr Thr Ile Pro Asp Gly Met Gly Ala Asn Ile
 450 455 460
 Pro Met Met Gly Thr His Met Pro Met Ala Gly Asp Met Asn Gly Leu

465 470 475 480
 Ser Pro Thr Gln Ala Leu Pro Pro Pro Leu Ser Met Pro Ser Thr Ser
 485 490 495
 His Cys Thr Pro Pro Pro Pro Tyr Pro Thr Asp Cys Ser Ile Val Ser
 500 505 510
 Phe Leu Ala Arg Leu Gly Cys Ser Ser Cys Leu Asp Tyr Phe Thr Thr
 515 520 525
 Gln Gly Leu Thr Thr Ile Tyr Gln Ile Glu His Tyr Ser Met Asp Asp
 530 535 540
 Leu Ala Ser Leu Lys Ile Pro Glu Gln Phe Arg His Ala Ile Trp Lys
 545 550 555 560
 Gly Ile Leu Asp His Arg Gln Leu His Glu Phe Ser Ser Pro Ser His
 565 570 575
 Leu Leu Arg Thr Pro Ser Ser Ala Ser Thr Val Ser Val Gly Ser Ser
 580 585 590
 Glu Thr Arg Gly Glu Arg Val Ile Asp Ala Val Arg Phe Thr Leu Arg
 595 600 605
 Gln Thr Ile Ser Phe Pro Pro Arg Asp Glu Trp Asn Asp Phe Asn Phe
 610 615 620
 Asp Met Asp Ala Arg Arg Asn Lys Gln Gln Arg Ile Lys Glu Glu Gly
 625 630 635 640
 Glu

<210> 7
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: p73-F1 sense primer

<400> 7
 tacgtgcacg taaagacacg ttgctcc

27

<210> 8
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: p73-R1 antisense primer

<400> 8
tgctgcacgt tgctccacgt ggacgtacg 29

<210> 9
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: p73-F2 sense primer

<400> 9
tacgtatact acgacgtgta cgtgaaggg 29

<210> 10
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: p73-R2 antisense primer

D7
<400> 10
atgaactacg acgtacgacg tccacgtat 29

W
<210> 11
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: HA-labeled expression construc

<400> 11
atgatccat atgatgttcc agattatgct 30

<210> 12
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: p51-F1 sense primer

<400> 12
aaagaaagtt attacccgatg 20

<210> 13
<211> 20

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: p51-R1 antisense primer

<400> 13
cgcggtggtct gtggttatagg 20

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: p51-F2 sense primer

<400> 14
catggaccag cagattcaga 20

D7
<210> 15
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: p51-R2 antisense primer

<400> 15
catcaccttg atctggatg 19

WIK
<210> 16
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: p51-F3 sense primer

<400> 16
ccacctggac gtattccact 20

<210> 17
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: p51-R3 antisense primer

<400> 17

tggtcataa.ggtaccag

18

<210> 18

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: p51-F4 sense primer

<400> 18

catgagctga gccgtgaat

19

<210> 19

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: p51-R4 antisense primer

<400> 19

tatcttcacg cgccttcctg

20

<210> 20

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: p51-F5 sense primer

<400> 20

atgaaccgcc gtccaatt

18

<210> 21

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: p51-R5 antisense primer

<400> 21

gtgctgagga aggtactgca

20

<210> 22

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: p51-F6 sense primer

<400> 22

tgaagatcaa agagtccttg

20

D7
<210> 23

<211> 20

<212> DNA

<213> Artificial Sequence

At
W
<220>

<223> Description of Artificial Sequence: p51-R6 antisense primer

<400> 23

ctagtggctt tgtgcctttg

20